

**RAW SEQUENCE LISTING**  
**ERROR REPORT**



A3

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/868,885

Source: Pt/09

Date Processed by STIC: 7/9/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.  
PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)  
PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**  
**VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/868,885

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, this will prevent "wrapping."
- 2      Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces
- 3      Misaligned Amino  
    Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers, use space characters, instead.
- 4      Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES) Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO: X (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: X (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES) Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present  
    in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.
- 11      Use of <220> Sequence(s) 44-45 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/868,885

DATE: 07/09/2001

TIME: 10:11:18

Input Set : A:\2584W00P.txt.txt

Output Set: N:\CRF3\07092001\I868885.raw

Does Not Comply  
Corrected Diskette Needed

P-6

3 <110> APPLICANT: Takeda Chemical Industries, Ltd.  
W--> 4 <120> TITLE OF INVENTION: Use of Peptide  
W--> 5 <130> FILE REFERENCE: 2584W00P  
C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/868,885  
C--> 6 <141> CURRENT FILING DATE: 2001-06-22  
6 <150> PRIOR APPLICATION NUMBER: JP 10-369585  
7 <151> PRIOR FILING DATE: 1998-12-25  
W--> 8 <160> NUMBER OF SEQ ID: 45  
11 <210> SEQ ID NO: 1  
12 <211> LENGTH: 98  
13 <212> TYPE: PRT  
14 <213> ORGANISM: Bovine  
W--> 15 <400> SEQUENCE: 1  
16 Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Gly Leu  
17 1 5 10 15  
18 Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile  
19 20 25 30  
20 Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg  
21 35 40 45  
22 Pro Val Gly Arg Phe Gly Arg Arg Ala Ala Pro Gly Asp Gly Pro  
23 50 55 60  
24 Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly  
25 65 70 75 80  
26 Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val  
27 85 90 95  
28 Gln Glu  
31 <210> SEQ ID NO: 2  
32 <211> LENGTH: 294  
33 <212> TYPE: DNA  
34 <213> ORGANISM: Bovine  
W--> 35 <400> SEQUENCE: 2  
C--> 36 atgaaggcgg tgggggcctg gctcctctgc ctgctgctgc tgggcctggc cctgcagggg 60  
37 gctgccagca gaggccacca gaactccatg gagatccgca cccccgacat caaccctgcc 120  
38 tggtagcgrg gcctgtggat ccggcccgct ggcgccttcg gcgcgggaag agctgccccy 180  
39 ggggacggac ccaggcctgg cccccggcgt gtgcgggect gcttcgcgct ggaaggcggy 240  
40 gctgagccct ccgagccct cccggggcgg ctgacggccc agctggtcca ggaa 294  
43 <210> SEQ ID NO: 3  
44 <211> LENGTH: 31  
45 <212> TYPE: PRT  
46 <213> ORGANISM: Bovine  
W--> 47 <400> SEQUENCE: 3  
48 Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn  
49 1 5 10 15  
50 Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe  
51 20 25 30  
53 <210> SEQ ID NO: 4  
54 <211> LENGTH: 32

all bases must be in lower case

↓

letters!

when  
using  
new sequence  
rules format

(global error)

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/868,885

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Input Set : A:\2584W00P.txt.txt

Output Set: N:\CRF3\07092001\I868885.raw

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55 <212> TYPE: PRT
56 <213> ORGANISM: Bovine
W--> 57 <400> SEQUENCE: 4
58 Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn
59 1 5 10 15
60 Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
61 20 25 30
63 <210> SEQ ID NO: 5
64 <211> LENGTH: 33
65 <212> TYPE: PRT
66 <213> ORGANISM: Bovine
W--> 67 <400> SEQUENCE: 5
68 Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn
69 1 5 10 15
70 Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
71 20 25 30
72 Arg
73 33
76 <210> SEQ ID NO: 6
77 <211> LENGTH: 20
78 <212> TYPE: PRT
79 <213> ORGANISM: Bovine
W--> 80 <400> SEQUENCE: 6
81 Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro
82 1 5 10 15
83 Val Gly Arg Phe
84 20
87 <210> SEQ ID NO: 7
88 <211> LENGTH: 21
89 <212> TYPE: PRT
90 <213> ORGANISM: Bovine
W--> 91 <400> SEQUENCE: 7
92 Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro
93 1 5 10 15
94 Val Gly Arg Phe Gly
95 20
98 <210> SEQ ID NO: 8
99 <211> LENGTH: 22
100 <212> TYPE: PRT
101 <213> ORGANISM: Bovine
W--> 102 <400> SEQUENCE: 8
103 Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro
104 1 5 10 15
105 Val Gly Arg Phe Gly Arg
106 20
109 <210> SEQ ID NO: 9
110 <211> LENGTH: 93
111 <212> TYPE: DNA
112 <213> ORGANISM: Bovine

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/868,885

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Input Set : A:\2584W00P.txt.txt

Output Set: N:\CRF3\07092001\I868885.raw

```

W--> 113 <400> SEQUENCE: 9
C--> 114 agcagagccc accagcactc catggagatc cgcacccccg acatcaaccc tgccctggtac 60
    115 gcrggccgtg ggaatccggcc cgtgggcccgc ttc 93
    118 <210> SEQ ID NO: 10
    119 <211> LENGTH: 96
    120 <212> TYPE: DNA
    121 <213> ORGANISM: Bovine
W--> 122 <400> SEQUENCE: 10
C--> 123 agcagagccc accagcactc catggagatc cgcacccccg acatcaaccc tgccctggtac 60
    124 gcrggccgtg ggaatccggcc cgtgggcccgc ttcggc 96
    127 <210> SEQ ID NO: 11
    128 <211> LENGTH: 99
    129 <212> TYPE: DNA
    130 <213> ORGANISM: Bovine
W--> 131 <400> SEQUENCE: 11
C--> 132 agcagagccc accagcactc catggagatc cgcacccccg acatcaaccc tgccctggtac 60
    133 gcrggccgtg ggaatccggcc cgtgggcccgc ttcggccgg 99
    136 <210> SEQ ID NO: 12
    137 <211> LENGTH: 60
    138 <212> TYPE: DNA
    139 <213> ORGANISM: Bovine
W--> 140 <400> SEQUENCE: 12
C--> 141 acccccagaca tcaacctgc ctggtacgcr ggcctggga tccggcccg gggccgcttc 60
    144 <210> SEQ ID NO: 13
    145 <211> LENGTH: 63
    146 <212> TYPE: DNA
    147 <213> ORGANISM: Bovine
W--> 148 <400> SEQUENCE: 13
C--> 149 acccccagaca tcaacctgc ctggtacgcr ggcctggga tccggcccg gggccgcttc 60
    150 ggc 63
    153 <210> SEQ ID NO: 14
    154 <211> LENGTH: 66
    155 <212> TYPE: DNA
    156 <213> ORGANISM: Bovine
W--> 157 <400> SEQUENCE: 14
C--> 158 acccccagaca tcaacctgc ctggtacgcr ggcctggga tccggcccg gggccgcttc 60
    159 ggcgg 66
    162 <210> SEQ ID NO: 15
    163 <211> LENGTH: 98
    164 <212> TYPE: PRS
    165 <213> ORGANISM: Bovine
W--> 166 <400> SEQUENCE: 15
    167 Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Gly Leu
    168 1 5 10 15
    169 Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile
    170 20 25 30
    171 Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg
    172 35 40 45
    173 Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Leu Gly Asp Gly Pro

```

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Input Set : A:\2584W00P.txt.txt

Output Set: N:\CRF3\07092001\I868885.raw

```

174      50      55      60
175 Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly
176      65      70      75      80
177 Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val
178      85      90      95
179 Gln Glu
182 <210> SEQ ID NO: 16
183 <211> LENGTH: 83
184 <212> TYPE: PRT
185 <213> ORGANISM: Rat
W--> 186 <400> SEQUENCE: 16
187 Met Ala Leu Lys Thr Trp Leu Leu Cys Leu Leu Leu Ser Leu Val
188      1      5      10      15
189 Leu Pro Gly Ala Ser Ser Arg Ala His Gln His Ser Met Glu Thr Arg
190      20      25      30
191 Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
192      35      40      45
193 Val Gly Arg Phe Gly Arg Arg Arg Ala Thr Pro Arg Asp Val Thr Gly
194      50      55      60
195 Leu Gly Gln Leu Ser Cys Leu Pro Leu Asp Gly Arg Thr Lys Phe Ser
196      65      70      75      80
197 Gln Arg Gly
200 <210> SEQ ID NO: 17
201 <211> LENGTH: 249
202 <212> TYPE: DNA
203 <213> ORGANISM: Rat
W--> 204 <400> SEQUENCE: 17
C--> 205 atggcctga agacgtgget tctgtgcttg ctgctgctaa gcttggtcct cccaggggct      60
206 tccagccgag ccaccacga ctccatggag acaagaaccc ctgatataaa tctgcctggg      120
207 tacacgggcc gcgggatcag gcctgtgggc cgcttcggca ggagagggc aaaccccgagg      180
208 gatgtcaactg gacttgcca actcagctgc ctccactgg atggacgcac caagtctctc      240
209 cagcgtgga
212 <210> SEQ ID NO: 18
213 <211> LENGTH: 31
214 <212> TYPE: PRT
215 <213> ORGANISM: Rat
W--> 216 <400> SEQUENCE: 18
217 Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn
218      1      5      10      15
219 Pro Ala Trp Trp Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe
220      20      25      30
223 <210> SEQ ID NO: 19
224 <211> LENGTH: 32
225 <212> TYPE: PRT
226 <213> ORGANISM: Rat
W--> 227 <400> SEQUENCE: 19
228 Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn
229      1      5      10      15
230 Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly

```

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Input Set : A:\2584W00P.txt.txt

Output Set : N:\CRF3\07092001\I868885.raw

```

231          20          25          30
234 <210> SEQ ID NO: 20
235 <211> LENGTH: 33
236 <212> TYPE: PRT
237 <213> ORGANISM: Rat
W--> 238 <400> SEQUENCE: 20
239 Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn
240 1          5          10          15
241 Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
242          20          25          30
243 Arg
246 <210> SEQ ID NO: 21
247 <211> LENGTH: 20
248 <212> TYPE: PRT
249 <213> ORGANISM: Rat
W--> 250 <400> SEQUENCE: 21
251 Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
252 1          5          10          15
253 Val Gly Arg Phe
254          20
257 <210> SEQ ID NO: 22
258 <211> LENGTH: 21
259 <212> TYPE: PRT
260 <213> ORGANISM: Rat
W--> 261 <400> SEQUENCE: 22
262 Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
263 1          5          10          15
264 Val Gly Arg Phe Gly
265          20
268 <210> SEQ ID NO: 23
269 <211> LENGTH: 22
270 <212> TYPE: PRT
271 <213> ORGANISM: Rat
W--> 272 <400> SEQUENCE: 23
273 Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
274 1          5          10          15
275 Val Gly Arg Phe Gly Arg
276          20
279 <210> SEQ ID NO: 24
280 <211> LENGTH: 93
281 <212> TYPE: DNA
282 <213> ORGANISM: Rat
W--> 283 <400> SEQUENCE: 24
C--> 284 agccgagcccc accagcactc catggagaca agaacccttg atatcaatcc tgcctggtac 60
285 acgggcccgcg ggaacaggcc tgtgggccgc ttc 93
288 <210> SEQ ID NO: 25
289 <211> LENGTH: 96
290 <212> TYPE: DNA
291 <213> ORGANISM: Rat

```

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<210> 44

<211> 31

<212> PRT

<213> Unknown

<220>

<221>

<223> Xaa on the 3rd position means Thr or Ala, Xaa on the 5th position means Arg or Gln, Xaa on the 10th position means Ile or Thr, Xaa on the 21st position means Thr or Ala, Xaa on the 22nd position means Gly or Ser.

<400> 44

Ser	Arg	Xaa	His	Xaa	His	Ser	Met	Glu	Xaa	Arg	Thr	Pro	Asp	Ile	Asn
1			5						10					15	
Pro	Ala	Trp	Tyr	Xaa	Xaa	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	
			20					25						30	

<210> 45

<211> 20

<212> PRT

<213> Unknown

<220>

<221>

<223> Xaa on the 10th position means Thr or Ala, Xaa on the 11th position means Gly or Ser.

<400> 45

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Xaa	Xaa	Arg	Gly	Ile	Arg	Pro
1				5					10					15	
Val	Gly	Arg	Phe												
			20												

*see item 11 on Ena Summary Sheet*

*same ena*



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/868,885

DATE: 07/09/2001

TIME: 10:11:19

Input Set : A:\2584WOOP.txt.txt

Output Set : N:\CRF3\07092001\I868885.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier  
 L:5 M:283 W: Missing Blank Line separator, <130> field identifier  
 L:6 M:270 C: Current Application Number differs, Replaced Current Application No  
 L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:8 M:283 W: Missing Blank Line separator, <160> field identifier  
 L:15 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:35 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:36 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=2  
 L:47 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:57 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:67 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:80 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:91 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:102 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:113 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:114 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=9  
 L:122 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:123 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=10  
 L:131 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:132 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=11  
 L:140 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:141 M:112 C: (48) String data converted to lower case,  
 L:148 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:149 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=13  
 L:157 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:158 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=14  
 L:166 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:186 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:204 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:205 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=17  
 L:216 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:227 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:238 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:250 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:261 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:272 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:283 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:284 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=24  
 L:292 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:293 M:112 C: (48) String data converted to lower case,

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/868,885

DATE: 07/09/2001  
TIME: 10:11:19

Input Set : A:\2584WOOP.txt.txt  
Output Set : N:\CRF3\07092001\I868885.raw

M:112 Repeated in SeqNo=25  
L:301 M:283 W: Missing Blank Line separator, <400> field identifier  
L:302 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=26  
L:310 M:283 W: Missing Blank Line separator, <400> field identifier  
L:311 M:112 C: (48) String data converted to lower case,  
L:318 M:283 W: Missing Blank Line separator, <400> field identifier  
L:319 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=28  
L:327 M:283 W: Missing Blank Line separator, <400> field identifier  
L:328 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=29  
L:336 M:283 W: Missing Blank Line separator, <400> field identifier  
L:355 M:283 W: Missing Blank Line separator, <400> field identifier  
L:356 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=31  
L:367 M:283 W: Missing Blank Line separator, <400> field identifier  
L:378 M:283 W: Missing Blank Line separator, <400> field identifier  
L:389 M:283 W: Missing Blank Line separator, <400> field identifier  
L:401 M:283 W: Missing Blank Line separator, <400> field identifier  
L:412 M:283 W: Missing Blank Line separator, <400> field identifier  
L:423 M:283 W: Missing Blank Line separator, <400> field identifier  
L:434 M:283 W: Missing Blank Line separator, <400> field identifier  
L:435 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=38  
L:443 M:283 W: Missing Blank Line separator, <400> field identifier  
L:444 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=39  
L:452 M:283 W: Missing Blank Line separator, <400> field identifier  
L:453 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=40  
L:461 M:283 W: Missing Blank Line separator, <400> field identifier  
L:462 M:112 C: (48) String data converted to lower case,  
L:469 M:283 W: Missing Blank Line separator, <400> field identifier  
L:470 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=42  
L:478 M:283 W: Missing Blank Line separator, <400> field identifier  
L:479 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=43  
L:487 M:283 W: Missing Blank Line separator, <220> field identifier  
L:488 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44  
L:490 M:283 W: Missing Blank Line separator, <400> field identifier  
L:491 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:44  
L:491 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44  
L:493 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:44  
L:493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44  
L:501 M:283 W: Missing Blank Line separator, <220> field identifier  
L:502 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45  
L:504 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/868,885

DATE: 07/09/2001

TIME: 10:11:19

Input Set : A:\2584WOOP.txt.txt

Output Set: N:\CRF3\07092001\I868885.raw

L:505 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:45  
L:505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45